Piero Giansanti

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

26 papers 1,480 h-index 27 g-index

27 1,807 11.3 4.45 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
26	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021 , 22, e53007	6.5	1
25	Systems approach reveals distinct and shared signaling networks of the four PGE receptors in T cells. <i>Science Signaling</i> , 2021 , 14, eabc8579	8.8	1
24	Identification of 7 000-9 000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LC-MS/MS. <i>Analytical Chemistry</i> , 2021 , 93, 8687-8692	7.8	9
23	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021 , 184, 3774-3793.e25	56.2	1
22	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020 , 48, D1153-D1163	20.1	67
21	Inhibition of the integrated stress response by viral proteins that block p-eIF2-eIF2B association. <i>Nature Microbiology</i> , 2020 , 5, 1361-1373	26.6	17
20	Dynamic remodelling of the human host cell proteome and phosphoproteome upon enterovirus infection. <i>Nature Communications</i> , 2020 , 11, 4332	17.4	7
19	Serine 25 phosphorylation inhibits RIPK1 kinase-dependent cell death in models of infection and inflammation. <i>Nature Communications</i> , 2019 , 10, 1729	17.4	69
18	Prostaglandin E2 signaling networks in T cells revealed through a systems approach. <i>FASEB Journal</i> , 2019 , 33, lb258	0.9	
17	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2387-2401	7.6	10
16	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) and (X)K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , 2017 , 16, 852-861	5.6	15
15	Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. <i>Nature Protocols</i> , 2016 , 11, 993-1006	18.8	245
14	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. <i>Cell Reports</i> , 2015 , 11, 1834-43	10.6	78
13	NF- B -Independent Role of IKK/IKKIIn Preventing RIPK1 Kinase-Dependent Apoptotic and Necroptotic Cell Death during TNF Signaling. <i>Molecular Cell</i> , 2015 , 60, 63-76	17.6	250
12	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. Journal of Proteome Research, 2015 , 14, 4332-41	5.6	48
11	Single-step enrichment by Ti4+-IMAC and label-free quantitation enables in-depth monitoring of phosphorylation dynamics with high reproducibility and temporal resolution. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2426-34	7.6	80
10	Evaluating the promiscuous nature of tyrosine kinase inhibitors assessed in A431 epidermoid carcinoma cells by both chemical- and phosphoproteomics. <i>ACS Chemical Biology</i> , 2014 , 9, 1490-8	4.9	14

LIST OF PUBLICATIONS

9	Phosphoproteomics-mediated identification of Fer kinase as a target of mutant Shp2 in Noonan and LEOPARD syndrome. <i>PLoS ONE</i> , 2014 , 9, e106682	3.7	7
8	Daily rhythms in the cyanobacterium synechococcus elongatus probed by high-resolution mass spectrometry-based proteomics reveals a small defined set of cyclic proteins. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2042-55	7.6	55
7	PZR coordinates Shp2 Noonan and LEOPARD syndrome signaling in zebrafish and mice. <i>Molecular and Cellular Biology</i> , 2014 , 34, 2874-89	4.8	25
6	Quantitative and qualitative proteome characteristics extracted from in-depth integrated genomics and proteomics analysis. <i>Cell Reports</i> , 2013 , 5, 1469-78	10.6	96
5	Interrogating cAMP-dependent kinase signaling in Jurkat T cells via a protein kinase A targeted immune-precipitation phosphoproteomics approach. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3350-	. 9 7.6	33
4	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. <i>Analyst, The</i> , 2012 , 137, 3541-8	5	41
3	Existence of hybrid structures in cationic liposome/DNA complexes revealed by their interaction with plasma proteins. <i>Colloids and Surfaces B: Biointerfaces</i> , 2011 , 82, 141-6	6	40
2	Recent developments in matrix solid-phase dispersion extraction. <i>Journal of Chromatography A</i> , 2010 , 1217, 2521-32	4.5	228
1	Liquid chromatography-negative ion atmospheric pressure photoionization tandem mass spectrometry for the determination of brominated flame retardants in environmental water and industrial effluents. <i>Journal of Chromatography A</i> , 2009 , 1216, 6400-9	4.5	41